

SEQUENCE LISTING

<110> INCYTE PHARMACEUTICALS, INC.
BANDMAN, Olga
TANG, Y. Tom
CORLEY, Neil C.
AZIMZAI, Yalda
BAUGHN, Mariah R.

<120> SCAD-RELATED MOLECULES

<130> PF-0559 PCT

<140> To Be Assigned

<141> Herewith

<150> 09/116,750; Unassigned

<151> 1998-07-16; 1998-07-16

<160> 6

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 278

<212> PRT

<213> HOMO SAPIENS

<220>

<221> misc_feature

<223> Incyte Clone No: 1240869

<300>

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Val Arg Met Ala Ser Ser Arg Met Thr Arg Arg Asp Pro Leu Thr Asn
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Lys Val Ala Leu Val Thr Ala Ser Thr Asp Gly Ile Gly Phe Ala Ile
35 40 45
Ala Arg Arg Leu Ala Gln Asp Arg Ala His Val Val Val Ser Ser Arg
50 55 60
Lys Gln Gln Asn Val Asp Gln Ala Val Ala Thr Leu Gln Gly Glu Gly
65 70 75 80
Leu Ser Val Thr Gly Thr Val Cys His Val Gly Lys Ala Glu Asp Arg
85 90 95
Glu Arg Leu Val Ala Thr Ala Val Lys Leu His Gly Gly Ile Asp Ile
100 105 110
Leu Val Ser Asn Ala Ala Val Asn Pro Phe Phe Gly Ser Ile Met Asp
115 120 125
Val Thr Glu Glu Val Trp Asp Lys Thr Leu Asp Ile Asn Val Lys Ala
130 135 140
Pro Ala Leu Met Thr Lys Ala Val Val Pro Glu Met Glu Lys Arg Gly
145 150 155 160
Gly Gly Ser Val Val Ile Val Ser Ser Ile Ala Ala Phe Ser Pro Ser
165 170 175
Pro Gly Phe Ser Pro Tyr Asn Val Ser Lys Thr Ala Leu Leu Gly Leu
180 185 190
Asn Asn Thr Leu Ala Ile Glu Leu Ala Pro Arg Asn Ile Arg Val Asn
195 200 205
Cys Leu Ala Pro Gly Leu Ile Lys Thr Ser Phe Ser Arg Met Leu Trp
210 215 220

Met Asp Lys Glu Lys Glu Glu Ser Met Lys Glu Thr Leu Arg Ile Arg
 225 230 235 240
 Arg Leu Gly Glu Pro Glu Asp Cys Ala Gly Ile Val Ser Phe Leu Cys
 245 250 255
 Ser Glu Asp Ala Ser Tyr Ile Thr Gly Glu Thr Val Val Val Gly Gly
 260 265 270
 Gly Thr Pro Ser Arg Leu
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<210> 2

<211> 564

<212> PRT

<213> HOMO SAPIENS

<220>

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<223> Incyte Clone No: 2060002

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<400> 2

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 Tyr Ala Tyr Pro Ser Asp Tyr Asp Met His Thr Gly Asp Pro Lys Gln
 20 25 30
 Asp Leu Ala Tyr Glu Arg Gln Tyr Glu Gln Gln Thr Tyr Gln Val Ile
 35 40 45
 Pro Glu Val Ile Lys Asn Phe Ile Gln Tyr Phe His Lys Thr Val Ser
 50 55 60
 Asp Leu Ile Asp Gln Lys Val Tyr Glu Leu Gln Ala Ser Arg Val Ser
 65 70 75 80
 Ser Asp Val Ile Asp Gln Lys Val Tyr Glu Ile Gln Asp Ile Tyr Glu
 85 90 95
 Asn Ser Trp Thr Lys Leu Thr Glu Arg Phe Phe Lys Asn Thr Pro Trp
 100 105 110
 Pro Glu Ala Glu Ala Ile Ala Pro Gln Val Gly Asn Asp Ala Val Phe
 115 120 125
 Leu Ile Leu Tyr Lys Glu Leu Tyr Tyr Arg His Ile Tyr Ala Lys Val
 130 135 140
 Ser Gly Gly Pro Ser Leu Glu Gln Arg Phe Glu Ser Tyr Tyr Asn Tyr
 145 150 155 160
 Cys Asn Leu Phe Asn Tyr Ile Leu Asn Ala Asp Gly Pro Ala Pro Leu
 165 170 175
 Glu Leu Pro Asn Gln Trp Leu Trp Asp Ile Ile Asp Glu Phe Ile Tyr
 180 185 190
 Gln Phe Gln Ser Phe Ser Gln Tyr Arg Cys Lys Thr Ala Lys Lys Ser
 195 200 205
 Glu Glu Glu Ile Asp Phe Leu Arg Ser Asn Pro Lys Ile Trp Asn Val
 210 215 220
 His Ser Val Leu Asn Val Leu His Ser Leu Val Asp Lys Ser Asn Ile
 225 230 235 240
 Asn Arg Gln Leu Glu Val Tyr Thr Ser Gly Gly Asp Pro Glu Ser Val
 245 250 255
 Ala Gly Glu Tyr Gly Arg His Ser Leu Tyr Lys Met Leu Gly Tyr Phe
 260 265 270
 Ser Leu Val Gly Leu Leu Arg Leu His Ser Leu Leu Gly Asp Tyr Tyr
 275 280 285
 Gln Ala Ile Lys Val Leu Glu Asn Ile Glu Leu Asn Lys Lys Ser Met
 290 295 300
 Tyr Ser Arg Val Pro Glu Cys Gln Val Thr Thr Tyr Tyr Tyr Val Gly
 305 310 315 320
 Phe Ala Tyr Leu Met Met Arg Arg Tyr Gln Asp Ala Ile Arg Val Phe
 325 330 335
 Ala Asn Ile Leu Leu Tyr Ile Gln Arg Thr Lys Ser Met Phe Gln Arg
 340 345 350

Thr Thr Tyr Lys Tyr Glu Met Ile Asn Lys Gln Asn Glu Gln Met His
 355 360 365
 Ala Leu Leu Ala Ile Ala Leu Thr Met Tyr Pro Met Arg Ile Asp Glu
 370 375 380
 Ser Ile His Leu Gln Leu Arg Glu Lys Tyr Gly Asp Lys Met Leu Arg
 385 390 395 400
 Met Gln Lys Gly Asp Pro Gln Val Tyr Glu Glu Leu Phe Ser Tyr Ser
 405 410 415
 Cys Pro Lys Phe Leu Ser Pro Val Val Pro Asn Tyr Asp Asn Val His
 420 425 430
 Pro Asn Tyr His Lys Glu Pro Phe Leu Gln Gln Leu Lys Val Phe Ser
 435 440 445
 Asp Glu Val Gln Gln Gln Ala Gln Leu Ser Thr Ile Arg Ser Phe Leu
 450 455 460
 Lys Leu Tyr Thr Thr Met Pro Val Ala Lys Leu Ala Gly Phe Leu Asp
 465 470 475 480
 Leu Thr Glu Gln Glu Phe Arg Ile Gln Leu Leu Val Phe Lys His Lys
 485 490 495
 Met Lys Asn Leu Val Trp Thr Ser Gly Ile Ser Ala Leu Asp Gly Glu
 500 505 510
 Phe Gln Ser Ala Ser Glu Val Asp Phe Tyr Ile Asp Lys Asp Met Ile
 515 520 525
 His Ile Ala Asp Thr Lys Val Ala Arg Arg Tyr Gly Asp Phe Phe Ile
 530 535 540
 Arg Gln Ile His Lys Phe Glu Glu Leu Asn Arg Thr Leu Lys Lys Met
 545 550 555 560
 Gly Gln Arg Pro

<210> 3
 <211> 1280
 <212> DNA
 <213> HOMO SAPIENS

<220>
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 <223> Incyte Clone No: 1240869

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acaaataagg	tggccctggt	aacggcctcc	accgacggga	tcggcttcgc	catcgcccg	180
cgtttgccc	aggacagggc	ccacgtggtc	gtcagcagcc	ggaagcagca	gaatgtggac	240
caggcggtg	ccacgctgca	gggggagggg	ctgagcgtga	cgggcaccgt	gtgccatgtg	300
gggaaggcgg	aggaccggga	gcggctgggtg	gccacggctg	tgaagcttca	tggaggtatc	360
gatatcctag	tctccaatgc	tgctgtcaac	cctttctttg	gaagcataat	ggatgtcact	420
gaggaggtgt	gggacaagac	tctggacatt	aatgtgaagg	ccccagccct	gatgacaaag	480
gcagtgggtgc	cagaaatgga	gaaacgagga	ggcggtcag	tggtgatcgt	gtcttcata	540
gcagccttca	gtccatctcc	tggttcagt	ccttacaatg	tcagtataaac	agccttgctg	600
ggcctcaaca	ataccctggc	catagagctg	gccccaaagg	acattagggt	gaactgccta	660
gcacctggac	ttatcaagac	tagcttcagc	aggatgctct	ggatggacaa	ggaaaaagag	720
gaaagcatga	aagaaaccct	gcggataaga	aggttaggcg	agccagagga	ttgtgctggc	780
atcgtgtctt	tcctgtgctc	tgaagatgcc	agctacatca	ctggggaaac	agtgggtggtg	840
ggtggaggaa	ccccgtccc	cctctgagga	ccgggagaca	gcccacaggc	cagagttggg	900
ctctagctcc	tggtgctgtt	cctgcattca	cccactggcc	tttcccacct	ctgctcacct	960
tactgttcac	ctcatcaaat	cagttctgcc	ctgtgaaaag	atccagcctt	ccctgccgtc	1020
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gagaacacag	gacaggcctg	ctgacaaggc	tgagtctacc	ttggcaaaga	ccaagatatt	1140
ttttcctggg	ccactgggga	atctgagggg	tgatgggaga	gaaggaaacct	ggagtgggaag	1200
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<210> 4

<211> 1894
 <212> DNA
 <213> HOMO SAPIENS

<220>
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 <223> Incyte Clone No: 2060002

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gcttatgaac gtcagtatga acagcaaaccc tatcagggtga tccctgaggt gatcaaaaac      180
ttcatccagt atttccacaa aactgtctca gatttgattg accagaaagt gtatgagcta      240
caggccagtc gtgtctccag tgatgtcatt gaccagaagg tgtatgagat ccaggacatc      300
tatgagaaca gctggaccaaa gctgactgaa agattcttca agaatacacc ttggcccagag      360
gctgaagcca ttgctccaca ggttggcaat gatgctgtct tcctgatttt atacaaagaa      420
ttatactaca ggcacatata tgccaaagtc agtgggggac cttccttggg gcagagggttt      480
gaatcctatt acaactactg caatctcttc aactacattc ttaatgccga tggctctgct      540
ccccttgaac tacccaacca gtggctctgg gatattatcg atgagttcat ctaccagttt      600
cagtcattca gtcagtaccg ctgtaagact gccagaagat cagaggagga gattgacctt      660
cttcgttcca atcccaaaaat ctggaatggt catagtgtcc tcaatgtcct tcattcccctg      720
gtagacaaat ccaacatcaa ccgacagttg gaggtatata caagcggagg tgacctgag      780
agtgtggctg gggagtatgg gcggcactcc ctctacaaaa tgcttggtta cttcagcctg      840
gtcgggcttc tccgcctgca ctccctgtta ggagattact accaggccat caaggtgctg      900
gagaacatcg aactgaacaa gaagagtatg tattcccgtg tgccagagtg ccaggtcacc      960
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gtcttcgcca acatcctcct ctacatccag aggaccaaga gcatgttcca gaggaccacg      1080
tacaagtatg agatgattaa caagcagaat gagcagatgc atgcgctgct ggccattgcc      1140
ctcacgatgt accccatgcg tatcgatgag agcattcacc tccagctgcg ggagaaatat      1200
ggggacaaga tgttgcgcat gcagaaaggt gaccacaaag tctatgaaga acttttcagt      1260
tactcctgcc ccaagttcct gtcgcctgta gtgcccact atgataatgt gcaccccaac      1320
taccacaaag agcccttcct gcagcagctg aaggtgtttt ctgatgaagt acagcagcag      1380
gccagctttt caaccatccg cagcttcctg aagctctaca ccaccatgcc tgtggccaag      1440
ctggctggct tcctggacct cacagagcag gagttccgga tccagcttct tgtcttcaaa      1500
cacaagatga agaaccctcg gtggaccagc ggtatctcag ccctggatgg tgaatttcag      1560
tcagcctcag aggttgactt ctacattgat aaggacatga tccacatcgc ggacaccaag      1620
gtcgccaggc gttatgggga tttcttcac cgtcagatcc acaaatttga ggagcttaat      1680
cgaaccctga agaagatggg acagagacct tgatgatatt cacacacatt caggaacctg      1740
ttttgatgta ttataggcag gaagtgtttt tgctaccgtg aaacctttac ctagatcagc      1800
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<210> 5
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 <212> PRT
 <213> HOMO SAPIENS

<300>

<308> g1079566

<400> 5

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 20          25          30
Val Leu Ala Asn Arg Val Ala Val Val Thr Gly Ser Thr Ser Gly Ile
 35          40          45
Gly Phe Ala Ile Ala Arg Arg Leu Ala Arg Asp Gly Ala His Val Val
 50          55          60
Ile Ser Ser Arg Lys Gln Gln Asn Val Asp Arg Ala Met Ala Lys Leu
 65          70          75          80
Gln Gly Glu Gly Leu Ser Val Ala Gly Ile Val Cys His Val Gly Lys
 85          90          95

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Ala Glu Asp Arg Glu Gln Leu Val Ala Lys Ala Leu Glu His Cys Gly
 100 105 110
 Gly Val Asp Phe Leu Val Cys Ser Ala Gly Val Asn Pro Leu Val Gly
 115 120 125
 Ser Thr Leu Gly Thr Ser Glu Gln Ile Trp Asp Lys Ile Leu Ser Val
 130 135 140
 Asn Val Lys Ser Pro Ala Leu Leu Leu Ser Gln Leu Leu Pro Tyr Met
 145 150 155 160
 Glu Asn Arg Arg Gly Ala Val Ile Leu Val Ser Ser Ile Ala Ala Tyr
 165 170 175
 Asn Pro Val Val Ala Leu Gly Val Tyr Asn Val Ser Lys Thr Ala Leu
 180 185 190
 Leu Gly Leu Thr Arg Thr Leu Ala Leu Glu Leu Ala Pro Lys Asp Ile
 195 200 205
 Arg Val Asn Cys Val Val Pro Gly Ile Ile Lys Thr Asp Phe Ser Lys
 210 215 220
 Val Phe His Gly Asn Glu Ser Leu Trp Lys Asn Phe Lys Glu His His
 225 230 235 240
 Gln Leu Gln Arg Ile Gly Glu Ser Glu Asp Cys Ala Gly Ile Val Ser
 245 250 255
 Phe Leu Cys Ser Pro Asp Ala Ser Tyr Val Asn Gly Glu Asn Ile Ala
 260 265 270
 Val Ala Gly Tyr Ser Thr Arg Leu
 275 280

<210> 6
 <211> 938
 <212> PRT
 <213> CAENORHABDITIS ELEGANS

<300>
 <308> g2731377

<400> 6
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 Glu Val Ala Asp Tyr Leu Val Tyr Phe Ser Arg Met Val Asp Glu Gln
 35 40 45
 Asn Val Pro Glu Ile Leu Thr Leu Tyr Asp Gln Ala Phe Pro Asp Leu
 50 55 60
 Thr Glu Arg Phe Phe Arg Asp Arg Met Trp Pro Asp Glu Asn Val Val
 65 70 75 80
 Glu Arg Ile Ile Gly Pro Gly Asn Lys Leu Phe Ile Ile Leu Tyr Lys
 85 90 95
 Glu Leu Tyr Tyr Arg Gln Leu Tyr Ala Arg Asn Thr Arg Gly Pro Leu
 100 105 110
 Leu Val His Arg Tyr Glu Ser Phe Met Asn Tyr Gln Glu Leu Phe Ser
 115 120 125
 Glu Leu Leu Ser Ser Lys Asp Pro Ile Pro Leu Ser Leu Pro Asn Val
 130 135 140
 Trp Leu Trp Asp Ile Ile Asp Glu Phe Val Tyr Gln Phe Gln Ala Phe
 145 150 155 160
 Cys Leu Tyr Lys Ala Asn Pro Gly Lys Arg Asn Ala Asp Glu Val Glu
 165 170 175
 Asp Leu Ile Asn Ile Glu Glu Asn Gln Asn Ala Trp Asn Ile Tyr Pro
 180 185 190
 Val Leu Asn Ile Leu Tyr Ser Leu Leu Ser Lys Ser Gln Ile Val Glu
 195 200 205
 Gln Leu Lys Ala Leu Lys Glu Lys Arg Asn Pro Asp Ser Val Ala Asp
 210 215 220
 Glu Phe Gly Gln Ser Asp Leu Tyr Phe Lys Leu Gly Tyr Phe Ala Leu
 225 230 235 240
 Ile Gly Leu Leu Arg Thr His Val Leu Leu Gly Asp Tyr His Gln Ala

245 250 255
 Leu Lys Thr Val Gln Tyr Val Asp Ile Asp Pro Lys Gly Ile Tyr Asn
 260 265 270
 Thr Val Pro Thr Cys Leu Val Thr Leu His Tyr Phe Val Gly Phe Ser
 275 280 285
 His Leu Met Met Arg Asn Tyr Gly Glu Ala Thr Lys Met Phe Val Asn
 290 295 300
 Cys Leu Leu Tyr Ile Gln Arg Thr Lys Ser Val Gln Asn Gln Gln Pro
 305 310 315 320
 Ser Lys Lys Asn Phe Gln Tyr Asp Val Ile Gly Lys Thr Trp Asp Gln
 325 330 335
 Leu Phe His Leu Leu Ala Ile Cys Leu Ala Ile Gln Pro Gln Arg Ile
 340 345 350
 Asp Glu Ser Ile Ala Ser Gln Leu Ser Glu Arg Cys Gly Glu Arg Met
 355 360 365
 Met His Met Ala Asn Gly Asn Ile Asp Glu Phe Arg Asn Ala Phe Ala
 370 375 380
 Thr Gly Cys Pro Lys Phe Leu Ser Pro Thr Thr Val Val Tyr Glu Gly
 385 390 395 400
 Val Asn Gln Ser Lys Glu Pro Leu Leu Arg Gln Thr Gln Ser Phe Leu
 405 410 415
 Glu Gly Ile Glu Ser Gln Met Ala Leu Pro Val Leu Arg Gly Tyr Leu
 420 425 430
 Lys Leu Tyr Thr Thr Leu Pro Thr Lys Lys Leu Ala Ser Phe Met Asp
 435 440 445
 Val Asp Asp Glu His Tyr Asp Ser Phe Ile Gly Lys Leu Leu Thr Tyr
 450 455 460
 Lys Met Ile Val Asn Glu Leu Gly Lys Glu Ala Gly Pro Ser Ser Ala
 465 470 475 480
 Asp Asp Asp Glu Pro Gln Thr Asp Ile Asp Phe Tyr Val Asp Arg Asp
 485 490 495
 Met Ile Asn Ile Ala Asp Thr Lys Val Ala Arg His Val Gly Cys Ala
 500 505 510
 Gln Thr Thr Arg Tyr Pro Glu Thr Met Ile Leu Lys Lys Phe Val
 515 520 525
 Gly Arg Thr Val Leu Ile Thr Gly Ala Ser Arg Gly Ile Gly Lys Glu
 530 535 540
 Ile Ala Leu Lys Leu Ala Lys Asp Gly Ala Asn Ile Val Val Ala Ala
 545 550 555 560
 Lys Thr Ala Thr Ala His Pro Lys Leu Pro Gly Thr Ile Tyr Ser Ala
 565 570 575
 Ala Glu Glu Ile Glu Lys Ala Gly Gly Lys Ala Leu Pro Cys Ile Val
 580 585 590
 Asp Val Arg Asp Glu Ala Ser Val Lys Ala Ser Val Glu Glu Ala Val
 595 600 605
 Lys Lys Phe Gly Gly Ile Asp Ile Leu Ile Asn Asn Ala Ser Ala Ile
 610 615 620
 Ser Leu Thr Asp Thr Glu Asn Thr Glu Met Lys Arg Tyr Asp Leu Met
 625 630 635 640
 His Ser Ile Asn Thr Arg Gly Thr Phe Leu Met Thr Lys Thr Cys Leu
 645 650 655
 Pro Tyr Leu Lys Ser Gly Lys Asn Pro His Val Leu Asn Ile Ser Pro
 660 665 670
 Pro Leu Leu Met Glu Thr Arg Trp Phe Ala Asn His Val Ala Tyr Thr
 675 680 685
 Met Ala Lys Tyr Gly Met Ser Met Cys Val Leu Gly Gln His Glu Glu
 690 695 700
 Phe Arg Pro His Gly Ile Ala Val Asn Ala Leu Trp Pro Leu Thr Ala
 705 710 715 720
 Ile Trp Thr Ala Ala Met Glu Met Leu Ser Asp Lys Gly Gly Glu Ala
 725 730 735
 Gly Ser Arg Lys Pro Ser Ile Met Ala Asp Ala Ala Tyr Ala Val Leu
 740 745 750
 Ser Lys Asn Ser Lys Asp Phe Thr Gly Asn Phe Cys Ile Asp Glu Asp
 755 760 765

Ile Leu Lys Ala Glu Gly Val Thr Asp Phe Asp Arg Tyr Ala Cys Val
770 775 780
Pro Asp Ala Pro Leu Met Pro Asp Phe Phe Ile Pro Ala Gly Thr Tyr
785 790 795 800
Asp His Lys Phe Ser Ser Gly Ala Gln Ile Gly Lys Lys Asn Lys Thr
805 810 815
His Glu Ala Gly Val Val Glu Glu Glu Ile Lys Gln Ile Phe Thr Ser
820 825 830
Ala Lys Arg Leu Leu Asn Ala Asp Ile Val Lys Lys Thr Gly Phe Val
835 840 845
Tyr Glu Phe Leu Leu Lys Asp Pro Thr Thr Lys Ser Glu Arg Ile Ile
850 855 860
Thr Leu Asp Leu Lys Asn Gly Glu Gly Ala Leu Thr Asp Lys Lys Ala
865 870 875 880
Ser Gly Lys Ala Asp Val Lys Phe Thr Leu Ala Pro Glu His Phe Ala
885 890 895
Pro Leu Phe Thr Gly Lys Leu Arg Pro Thr Thr Ala Leu Met Thr Lys
900 905 910
Lys Leu Gln Ile Ser Gly Asp Met Pro Gly Ala Met Lys Leu Glu Ser
915 920 925
Leu Leu Arg Lys Phe Thr Glu Gly Lys Leu
930 935